STIC Biotechnology Systems Branch

RAW SEQUENCE LISTING
ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: _10/534,788_

Source: _PCT/10_

Date Processed by STIC: _5/23/05_

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY
FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER VERSION 4.2.2 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:
          http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.
Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.
Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio **(<http://www.uspto.gov/ebc/efs/downloads/documents.htm>** , **EFS Submission User Manual** - ePAVE)
2. **U.S. Postal Service:** Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. **Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05):**
   U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314

Revised 01/24/05

Raw Sequence Listing Error Summary

ERROR DETECTED	SUGGESTED CORRECTION	SERIAL NUMBER: *10/534,788*

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 ____ Wrapped Nucleics
Wrapped Aminos
The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."

·2 ____ Invalid Line Length
The rules require that a line not exceed 72 characters in length. This includes white spaces.

3 ____ Misaligned Amino
Numbering
The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.

4 ____ Non-ASCII
The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.

56-57

5 ____ Variable Length
Sequence(s) ____ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.

6 ____ PatentIn 2.0
"bug"
A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.

7 ____ Skipped Sequences
(OLD RULES)
Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i)   SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.

8 ____ Skipped Sequences
(NEW RULES)
Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence.
<210> sequence id number
<400> sequence id number
000

9 ____ Use of n's or Xaa's
(NEW RULES)
Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

10 ____ Invalid <213>
Response
Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence

11 ____ Use of <220>
Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32)   (Sec. 1.823 of Sequence Rules)

FYI

12 ____ PatentIn 2.0
"bug"
Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

13 ____ Misuse of n/Xaa
"n" can only represent a single <u>nucleotide</u>; "Xaa" can only represent a single <u>amino acid</u>

AMC – Biotechnology Systems Branch – 09/09/2003

PCT

RAW SEQUENCE LISTING   DATE: 05/23/2005
PATENT APPLICATION: US/10/534,788   TIME: 13:47:31

Input Set : D:\VOSS007.txt
Output Set: N:\CRF4\05232005\J534788.raw

```
 3 <110> APPLICANT: BAUERLE, PATRICK
 4       HOFFMANN, PATRICK
 5       WEINBERGER, SUSANNE
 6       KISCHEL, ROMAN
 8 <120> TITLE OF INVENTION: METHOD FOR IDENTIFIYING ANTIGEN SPECIFIC B CELLS
10 <130> FILE REFERENCE: VOSS:007US
12 <140> CURRENT APPLICATION NUMBER: US/10/534,788
13 <141> CURRENT FILING DATE: 2005-05-13
15 <150> PRIOR APPLICATION NUMBER: PCT/EP2003/012664
16 <151> PRIOR FILING DATE: 2003-11-12
18 <160> NUMBER OF SEQ ID NOS: 89
20 <170> SOFTWARE: PatentIn version 3.1
22 <210> SEQ ID NO: 1
23 <211> LENGTH: 21
24 <212> TYPE: DNA
25 <213> ORGANISM: artificial sequence
27 <220> FEATURE:
28 <223> OTHER INFORMATION: mus musculus primer
30 <400> SEQUENCE: 1
31 accttcaaca ccccagccat g                                21
34 <210> SEQ ID NO: 2
35 <211> LENGTH: 23
36 <212> TYPE: DNA
37 <213> ORGANISM: artificial sequence
39 <220> FEATURE:
40 <223> OTHER INFORMATION: mus musculus primer
42 <400> SEQUENCE: 2
43 gctcggtcag gatcttcatg agg                              23
46 <210> SEQ ID NO: 3
47 <211> LENGTH: 20
48 <212> TYPE: DNA
49 <213> ORGANISM: artificial sequence
51 <220> FEATURE:
52 <223> OTHER INFORMATION: mus musculus primer
54 <400> SEQUENCE: 3
55 gctacacatt cagtagcttc                                  20
58 <210> SEQ ID NO: 4
59 <211> LENGTH: 20
60 <212> TYPE: DNA
61 <213> ORGANISM: artificial sequence
63 <220> FEATURE:
64 <223> OTHER INFORMATION: mus musculus primer
66 <400> SEQUENCE: 4
```

C--> (line 12)

Does Not Comply
Corrected Diskette Neede'

PP.2,6-8

5/23/05

```
 67 gtatggcatg tttaccatcg                                              20
 70 <210> SEQ ID NO: 5
 71 <211> LENGTH: 20
 72 <212> TYPE: DNA
 73 <213> ORGANISM: artificial sequence
 75 <220> FEATURE:
 76 <223> OTHER INFORMATION: mus musculus primer
 78 <400> SEQUENCE: 5
 79 tcagtagctt ctggatagag
 82 <210> SEQ ID NO: 6
 83 <211> LENGTH: 26                                                   20
 84 <212> TYPE: DNA
C--> 85 <213> ORGANISM: artificial primer
W--> 87 <220> FEATURE:
W--> 87 <223> OTHER INFORMATION:
W--> 87 <400> 6
 88 gtatggcatg tttaccatcg tattac                                       26
 91 <210> SEQ ID NO: 7
 92 <211> LENGTH: 20
 93 <212> TYPE: DNA
 94 <213> ORGANISM: artificial sequence
 96 <220> FEATURE:
 97 <223> OTHER INFORMATION: mus musculus primer
 99 <400> SEQUENCE: 7                                                  20
100 gttacaattt ctccgacaag
103 <210> SEQ ID NO: 8
104 <211> LENGTH: 20
105 <212> TYPE: DNA
106 <213> ORGANISM: artificial sequence
108 <220> FEATURE:
109 <223> OTHER INFORMATION: mus musculus primer
111 <400> SEQUENCE: 8                                                  20
112 gtcgcaggcg gaataatcac
115 <210> SEQ ID NO: 9
116 <211> LENGTH: 20
117 <212> TYPE: DNA
118 <213> ORGANISM: artificial sequence
120 <220> FEATURE:
121 <223> OTHER INFORMATION: mus musculus primer
123 <400> SEQUENCE: 9                                                  20
124 tctccgacaa gtggattcac
127 <210> SEQ ID NO: 10
128 <211> LENGTH: 20
129 <212> TYPE: DNA
130 <213> ORGANISM: artificial sequence
132 <220> FEATURE:
133 <223> OTHER INFORMATION: mus musculus primer
135 <400> SEQUENCE: 10                                                 20
136 gcaggcggaa taatcacccg
```

Handwritten annotations: Invalid <213> response. See item 10 on Error Summary sheet.

Handwritten annotation (pointing to section): This section is mandatory if <213> response is "Artificial Sequence"

Input Set : D:\VOSS007.txt
Output Set: N:\CRF4\05232005\J534788.raw

```
139 <210> SEQ ID NO: 11
140 <211> LENGTH: 21
141 <212> TYPE: DNA
142 <213> ORGANISM: artificial sequence
144 <220> FEATURE:
145 <223> OTHER INFORMATION: homo sapiens primer
147 <400> SEQUENCE: 11
148 tggcagatga gcttggactt g                                          21
151 <210> SEQ ID NO: 12
152 <211> LENGTH: 21
153 <212> TYPE: DNA
154 <213> ORGANISM: artificial sequence
156 <220> FEATURE:
157 <223> OTHER INFORMATION: homo sapiens primer
159 <400> SEQUENCE: 12
160 acactctccc ctgttgaagc t                                          21
163 <210> SEQ ID NO: 13
164 <211> LENGTH: 20
165 <212> TYPE: DNA
166 <213> ORGANISM: artificial sequence
168 <220> FEATURE:
169 <223> OTHER INFORMATION: homo sapiens primer
171 <400> SEQUENCE: 13
172 gtgctccctt catgcgtgac                                            20
175 <210> SEQ ID NO: 14
176 <211> LENGTH: 21
177 <212> TYPE: DNA
178 <213> ORGANISM: artificial sequence
180 <220> FEATURE:
181 <223> OTHER INFORMATION: homo sapiens primer
183 <400> SEQUENCE: 14
184 actcgtcata ctcctgcttg c                                          21
187 <210> SEQ ID NO: 15
188 <211> LENGTH: 24
189 <212> TYPE: DNA
190 <213> ORGANISM: artificial sequence
192 <220> FEATURE:
193 <223> OTHER INFORMATION: homo sapiens primer
195 <400> SEQUENCE: 15
196 tggaagaggc acgttctttt cttt                                       24
199 <210> SEQ ID NO: 16
200 <211> LENGTH: 20
201 <212> TYPE: DNA
202 <213> ORGANISM: artificial sequence
204 <220> FEATURE:
205 <223> OTHER INFORMATION: homo sapiens primer
207 <400> SEQUENCE: 16
208 agttacccga ttggagggcg                                            20
211 <210> SEQ ID NO: 17
```

```
212 <211> LENGTH: 19
213 <212> TYPE: DNA
214 <213> ORGANISM: artificial sequence
216 <220> FEATURE:
217 <223> OTHER INFORMATION: homo sapiens primer
219 <400> SEQUENCE: 17                                          19
220 ccttccaggc cactgtcac
223 <210> SEQ ID NO: 18
224 <211> LENGTH: 20
225 <212> TYPE: DNA
226 <213> ORGANISM: artificial sequence
228 <220> FEATURE:
229 <223> OTHER INFORMATION: homo sapiens primer
231 <400> SEQUENCE: 18                                          20
232 gtggggcgcc ccaggcacca
235 <210> SEQ ID NO: 19
236 <211> LENGTH: 23
237 <212> TYPE: DNA
238 <213> ORGANISM: artificial sequence
240 <220> FEATURE:
241 <223> OTHER INFORMATION: homo sapiens primer
243 <400> SEQUENCE: 19                                          23
244 gatggaggcg gcgatccaca cgg
247 <210> SEQ ID NO: 20
248 <211> LENGTH: 23
249 <212> TYPE: DNA
250 <213> ORGANISM: artificial sequence
252 <220> FEATURE:
253 <223> OTHER INFORMATION: homo sapiens primer
255 <400> SEQUENCE: 20                                          23
256 cagrtgcagc tggtgcartc tgg
259 <210> SEQ ID NO: 21
260 <211> LENGTH: 23
261 <212> TYPE: DNA
262 <213> ORGANISM: artificial sequence
264 <220> FEATURE:
265 <223> OTHER INFORMATION: homo sapiens primer
267 <400> SEQUENCE: 21                                          23
268 saggtccagc tggtrcagtc tgg
271 <210> SEQ ID NO: 22
272 <211> LENGTH: 23
273 <212> TYPE: DNA
274 <213> ORGANISM: artificial sequence
276 <220> FEATURE:
277 <223> OTHER INFORMATION: homo sapiens primer
279 <400> SEQUENCE: 22                                          23
280 caggtccagc ttgtacagtc tgg
283 <210> SEQ ID NO: 23
284 <211> LENGTH: 23
```

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/534,788

DATE: 05/23/2005
TIME: 13:47:31

Input Set : D:\VOSS007.txt
Output Set: N:\CRF4\05232005\J534788.raw

```
285 <212> TYPE: DNA
286 <213> ORGANISM: artificial sequence
288 <220> FEATURE:
289 <223> OTHER INFORMATION: homo sapiens primer
291 <400> SEQUENCE: 23
292 sagrtcacct tgaaggagtc tgg                                        23
295 <210> SEQ ID NO: 24
296 <211> LENGTH: 23
297 <212> TYPE: DNA
298 <213> ORGANISM: artificial sequence
300 <220> FEATURE:
301 <223> OTHER INFORMATION: homo sapiens primer
303 <400> SEQUENCE: 24
304 saggtgcagc tggtggartc tgg                                        23
307 <210> SEQ ID NO: 25
308 <211> LENGTH: 23
309 <212> TYPE: DNA
310 <213> ORGANISM: artificial sequence
312 <220> FEATURE:
313 <223> OTHER INFORMATION: homo sapiens primer
315 <400> SEQUENCE: 25
316 gaggtgcagc tgktggagwc ygg                                        23
319 <210> SEQ ID NO: 26
320 <211> LENGTH: 23
321 <212> TYPE: DNA
322 <213> ORGANISM: artificial sequence
324 <220> FEATURE:
325 <223> OTHER INFORMATION: homo sapiens primer
327 <400> SEQUENCE: 26
328 cagctgcagc tacagcagtg ggg                                        23
331 <210> SEQ ID NO: 27
332 <211> LENGTH: 23
333 <212> TYPE: DNA
334 <213> ORGANISM: artificial sequence
336 <220> FEATURE:
337 <223> OTHER INFORMATION: homo sapiens primer
339 <400> SEQUENCE: 27
340 cagstgcagc tgcaggagtc sgg                                        23
343 <210> SEQ ID NO: 28
344 <211> LENGTH: 23
345 <212> TYPE: DNA
346 <213> ORGANISM: artificial sequence
348 <220> FEATURE:
349 <223> OTHER INFORMATION: homo sapiens primer
351 <400> SEQUENCE: 28
352 gargtgcagc tggtgcagtc tgg                                        23
355 <210> SEQ ID NO: 29
356 <211> LENGTH: 23
357 <212> TYPE: DNA
```

```
<210>  42
<211>  23   Artificial
<212>  DNA
<213>  artificdial sequence
```

see p. 8 for error explanation

```
<400>  42
cagccwgkgc tgactcagcc mcc                    23
```

```
<210>  56
<211>  31
<212>  DNA
<213>  artificial sequence

<220>
<223>  homo sapiens primer

<220>
<221>  misc_feature
<222>  (31)..(31)
<223>  n denotes a variable number of nucleotides which are part of the
        sequence of specific VL clones

<400>  56
ggagccgccg ccgccagaac caccaccacc n                                    31
```

variable length is not permitted (see item 5 on Error Summary Sheet)

If "indefinite" is intended, please state that on the <223> line

same error in Sequence 57

RAW SEQUENCE LISTING ERROR SUMMARY   DATE: 05/23/2005
PATENT APPLICATION: US/10/534,788   TIME: 13:47:32

Input Set : D:\VOSS007.txt
Output Set: N:\CRF4\05232005\J534788.raw

Please Note:
Use of n and/or Xaa have been detected in the Sequence Listing. Please review the
Sequence Listing to ensure that a corresponding explanation is presented in the <220>
to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:56; N Pos. 31
Seq#:57; N Pos. 34

Use of <220> Feature(NEW RULES):   *error explanation*
Sequence(s)__are missing the <220> Feature and associated headings.
Use of <220> to <223> is MANDATORY if <213> ORGANISM is "Artificial Sequence"
or"Unknown". Please explain source of genetic material in <220> to <223>
section (See "Federal Register," 6/01/98, Vol. 63, No. 104,pp.29631-32)
(Sec.1.823 of new Rules)

Seq#:6,42

Input Set : **D:\VOSS007.txt**
Output Set: **N:\CRF4\05232005\J534788.raw**

L:12 M:270 C: Current Application Number differs, Replaced Current Application Number
L:85 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:6
L:87 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:6, <213>
ORGANISM:Artificial Sequence
L:87 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:6, <213>
ORGANISM:Artificial Sequence
L:87 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:6,Line#:87
L:514 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:42
L:516 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:42, <213>
ORGANISM:Artificial Sequence
L:516 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:42, <213>
ORGANISM:Artificial Sequence
L:516 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:42,Line#:516
L:692 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:56 after pos.:0
L:711 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:57 after pos.:0